AMENDMENTS TO THE CLAIMS

This listing of claims replaces all prior versions, and listings, of claims in the application.

1. (Original) A method for identifying a candidate compound for treating, reducing, or preventing a pathogenic infection, said method comprising:

(a) contacting a pathogenic cell with a candidate compound; and

(b) measuring the production of a molecule selected from the group consisting of an 4-hydroxy-2-alkylquinoline (HAQ) molecule, 4-hydroxy-2-heptylquinoline (HHQ) molecule, or a derivative or precursor thereof in said cell, a candidate compound that reduces said production relative to production of said molecule by a cell not contacted with said candidate compound, identifying a candidate compound useful for treating, reducing, or preventing a pathogenic infection.

2. (Original) The method of claim 1, wherein step (b) comprises measuring the HAQ molecule.

3. (Original) The method of claim 1, wherein said pathogenic cell infects a mammal.

4. (Original) The method of claim 3, wherein said mammal is a human.

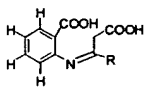
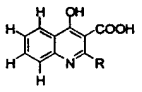
5. (Original) The method of claim 1, wherein said pathogenic cell infects a plant.

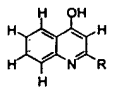
6. (Original) The method of claim 1, wherein said pathogenic cell is *Pseudomonas aeruginosa*.

7. (Original) The method of claim 6, wherein said *Pseudomonas aeruginosa* PA14 or PA01.

8. (Original) The method of claim 1, wherein said HAQ molecule, said HHQ molecule, or said derivative or precursor thereof is selected from any one of the molecules shown in Fig. 5 or Fig. 2.

9. (Original) The method of claim 8, wherein said molecule is selected from the group consisting of

 and  .

10. (Original) The method of claim 1, wherein said HHQ is  .

11. (Original) A method for identifying a candidate compound for treating, reducing, or preventing a pathogenic infection, said method comprising:

(a) contacting a population of cultured pathogenic cells with a candidate compound;

(b) collecting supernatant from said population of cultured pathogenic cells;

(c) contacting said collected supernatant with a second population of cells expressing a PqsH protein;

(d) measuring production of HHQ in said population of cells, a candidate compound that reduces said production relative to HHQ production in a population of cells contacted with supernatant collected from a population of cells that has not been contacted with said candidate compound, identifying a candidate compound useful for treating, reducing, or preventing a pathogenic infection.

12. (Original) The method of claim 11, wherein said pathogenic cells infect mammals.

13. (Original) The method of claim 12, wherein said mammal is a human.

14. (Original) The method of claim 11, wherein said pathogenic cells infect plants.

15. (Original) The method of claim 11, wherein said pathogenic cells are *Pseudomonas aeruginosa*.

16. (Original) The method of claim 15, wherein said *Pseudomonas aeruginosa* are *Pseudomonas aeruginosa* PA14 or *Pseudomonas aeruginosa* PAO1.

17. (Original) The method of claim 11, wherein said PqsH protein is encoded by a nucleic acid molecule substantially identical to the nucleic acid of SEQ ID NO:6 or by a nucleic acid molecule that binds under stringent conditions to SEQ ID NO:6 or a sequence complementary thereto.

18. (Original) The method of claim 11, wherein said PqsH protein is substantially identical to the amino acid sequence of SEQ ID NO:13.

19. (Original) The method of claim 11, wherein said PqsH protein is a *Pseudomonas aeruginosa* PqsH protein.

20-55. (Cancelled)